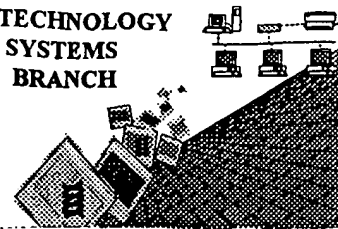


E.
Slobodiansky



RAW SEQUENCE LISTING ERROR REPORT

#17

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/830,111B
Source: 1600
Date Processed by STIC: 6/5/2003

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 4.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

<http://www.uspto.gov/web/offices/pac/checker>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<<http://www.uspto.gov/ebc/efs/downloads/documents.htm>> , EFS Submission User Manual - ePAVE)

2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450

3. Hand Carry directly to:

U.S. Patent and Trademark Office, Technology Center 1600, Reception Area, 7th Floor, Examiner Name, Sequence Information, Crystal Mall One, 1911 South Clark Street, Arlington, VA 22202

Or

U.S. Patent and Trademark Office, Box Sequence, Customer Window, Lobby, Room 1B03, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202

4. Federal Express, United Parcel Service, or other delivery service to: U.S. Patent and Trademark Office, Box Sequence, Room 1B03-Mailroom, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202

Revised 04/24/2003

Raw Sequence Listing Error Summary

17

ERROR DETECTED

SUGGESTED CORRECTION

SERIAL NUMBER: 09/830,111B

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 Wrapped Nucleics
 Wrapped Aminos The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."
- 2 Invalid Line Length The rules require that a line not exceed 72 characters in length. This includes white spaces.
- 3 Misaligned Amino
 Numbering The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.
- 4 Non-ASCII The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.
- 5 Variable Length Sequence(s) contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
- 6 PatentIn 2.0
 "bug" A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) . Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
- 7 Skipped Sequences
 (OLD RULES) Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence:
 (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
 (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
 (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
 This sequence is intentionally skipped

 Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.
- 8 Skipped Sequences
 (NEW RULES) Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence.
 <210> sequence id number
 <400> sequence id number
 000
- 9 Use of n's or Xaa's
 (NEW RULES) Use of n's and/or Xaa's have been detected in the Sequence Listing.
 Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
 In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 10 Invalid <213>
 Response Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence
- 11 Use of <220> Sequence(s) 3-8 missing the <220> "Feature" and associated numeric identifiers and responses.
 Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
 (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
- 12 PatentIn 2.0
 "bug" Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.
- 13 Misuse of n n can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represent any value not specifically a nucleotide.

Sequence listing

<110> Kaneka Corporation

<120> Process for producing coenzyme Q10

<130> T549/QX-GT2

<150> JP P1999-237561

<151> 1999-08-24

<160> 2 8 8 do not use underline's
delete 2

<210> 1

<211> 1653

<212> DNA

<213> Saioella complicata

<400> 1

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gagattgagt tcaggacaaa gctttgatcc gtgaggtcta catcttcagc aaatcatttc 120

aaatccatat acc atg gcc tca cca gca ctg cgg ata cga agc atc agc 169
Met Ala Ser Pro Ala Leu Arg Ile Arg Ser Ile Ser
1 5 10

tct cga tca atc gcc tct ctg cga tgg gtt acc cta aga aca gcc tgg 217
Ser Arg Ser Ile Ala Ser Leu Arg Ser Val Thr Leu Arg Thr Ala Ser
15 20 25

gca cct tca tta cga cta aga tgt acc cgg acg ago cgg cca tgg agt 265
Ala Pro Ser Leu Arg Leu Arg Cys Thr Pro Thr Ser Arg Pro Ser Ser
30 35 40

tca tgg get get get gtg tct tgg gcg tgg aga ctg gtt gag cct gat 313
Ser Trp Ala Ala Ala Val Ser Ser Ala Ser Arg Leu Val Glu Pro Asp
45 50 55 60

ccg aat caa cct ctc atc aat ccg ctc aac ttg gtc ggt ccc gag atg 361
Pro Asn Gln Pro Leu Ile Asn Pro Leu Asn Leu Val Gly Pro Glu Met
65 70 75

tca aat ctt aca tcc aac atc cga tct ctc ctc ggt tca gga cac cct 409
Ser Asn Leu Thr Ser Asn Ile Arg Ser Leu Leu Gly Ser Gly His Pro
80 85 90

tct ctc gac act gtc get aaa tac tat gtt cag tct gag gga aag cat 457
Ser Leu Asp Thr Val Ala Lys Tyr Tyr Val Gln Ser Glu Gly Lys His
95 100 105

att cgt cog ctc atg gta ctg ctg atg get cag gcg acg gag gtt gcg 505
Ile Arg Pro Leu Met Val Leu Leu Met Ala Gln Ala Thr Glu Val Ala
110 115 120

cca aaa gtt cag ggt tgg gag aag gtc gtc gag gtt ccg gtc aac gag 553
Pro Lys Val Gln Gly Trp Glu Lys Val Val Glu Val Pro Val Asn Glu
125 130 135 140

Does Not Comply
Corrected Diskette Needed

see pp 1, 4-5

#17

gga ctc gca cca cca gag gtg ctc aat gac aag aac cca gat atg atg	601
Gly Leu Ala Pro Pro Glu Val Leu Asn Asp Lys Asn Pro Asp Met Met	
145 150 155	
aac atg agg tca gga cca tta acg aag gac ggc gag atc gag gga cag	649
Asn Met Arg Ser Gly Pro Leu Thr Lys Asp Gly Glu Ile Glu Gly Gln	
160 165 170	
acg tcg aat atc ctc gcc tcg caa cgg cgg ttg get gag atc acg gag	697
Thr Ser Asn Ile Leu Ala Ser Gln Arg Arg Leu Ala Glu Ile Thr Glu	
175 180 185	
atg atc cat gca gca tca ctc ctc cac gac gac gtt atc gac get tcc	745
Met Ile His Ala Ala Ser Leu Leu His Asp Asp Val Ile Asp Ala Ser	
190 195 200	
gag acc aga cga aac gca cca tcc gga aac cag gca ttc gga aac aag	793
Glu Thr Arg Arg Asn Ala Pro Ser Gly Asn Gln Ala Phe Gly Asn Lys	
205 210 215 220	
atg gcg att ttg get ggt gat ttc ttg ttg gga cgg gcg tct gtt gca	841
Met Ala Ile Leu Ala Gly Asp Phe Leu Leu Gly Arg Ala Ser Val Ala	
225 230 235	
ttg gcg agg ttg cgc aat ccg gag gtg att gag ctt ttg get act gtt	889
Leu Ala Arg Leu Arg Asn Pro Glu Val Ile Glu Leu Leu Ala Thr Val	
240 245 250	
att gca aac ttg gtt gag gga gag ttc atg cag ttg aaa aat act gtt	937
Ile Ala Asn Leu Val Glu Gly Glu Phe Met Gln Leu Lys Asn Thr Val	
255 260 265	
gat gat gcg att gag get acg gcg acg cag gaa acg ttc gat tac tat	985
Asp Asp Ala Ile Glu Ala Thr Ala Thr Gln Glu Thr Phe Asp Tyr Tyr	
270 275 280	
ttg cag aag act tac ttg aag act gcg tcc ttg att gcc aag tcg tgc	1033
Leu Gln Lys Thr Tyr Leu Lys Thr Ala Ser Leu Ile Ala Lys Ser Cys	
285 290 295 300	
aga gca agt gcg ctt etg ggt ggt get acg ect gag gtt get gat get	1081
Arg Ala Ser Ala Leu Leu Gly Gly Ala Thr Pro Glu Val Ala Asp Ala	
305 310 315	
gct tat gct tac gga agg aac ctt ggt ttg gca ttc cag atc gtc gac	1129
Ala Tyr Ala Tyr Gly Arg Asn Leu Gly Leu Ala Phe Gln Ile Val Asp	
320 325 330	
gac atg ctc gac tac acc gtc tcc get acc gac ctc ggt aag ccc gcc	1177
Asp Met Leu Asp Tyr Thr Val Ser Ala Thr Asp Leu Gly Lys Pro Ala	
335 340 345	
ggt gca gac ctc cag ctc ggt ctc gcc acc gcg ccg gcc ctc ttc gca	1225
Gly Ala Asp Leu Gln Leu Gly Leu Ala Thr Ala Pro Ala Leu Phe Ala	
350 355 360	
tgg aag cac cac gcc gag ctc ggt ccc atg atc aag cgc aag ttc tct	1273
Trp Lys His His Ala Glu Leu Gly Pro Met Ile Lys Arg Lys Phe Ser	
365 370 375 380	

gac cca gga gac gtc gag cgt gca cgc gag ttg gtc gag aaa agt gat 1321
 Asp Pro Gly Asp Val Glu Arg Ala Arg Glu Leu Val Glu Lys Ser Asp
 385 390 395

gga ttg gag aag acg aga gcc ttg gcg gag gag tat gcc cag aag gcg 1369
 Gly Leu Glu Lys Thr Arg Ala Leu Ala Glu Glu Tyr Ala Gln Lys Ala
 400 405 410

ttg gat gca att cgg acg ttc ccg gag agt cog gca cgg aag get ttg 1417
 Leu Asp Ala Ile Arg Thr Phe Pro Glu Ser Pro Ala Arg Lys Ala Leu
 415 420 425

gag cag ttg acg gac aag gtg ttg act agg tca aga taggaattcgagct 1467
 Glu Gln Leu Thr Asp Lys Val Leu Thr Arg Ser Arg
 430 435 440

cggtacccgg ggatcctcta gagtcgacct gcaggcatgc aagcttggct gttttggcgg 1527

atgagagaag attttcagcc tgatacagat taaatcagaa cgcagaagcg gtctgataaa 1587

acagaatttg cctggcggca gtagcgcggg ggtccacct gaccccatgc cgaactcaga 1647

agtgaa 1653

<210> 2

<211> 440

<212> PRT

<213> Saioella complicata

<400> 2

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 Ile Ala Ser Leu Arg Ser Val Thr Leu Arg Thr Ala Ser Ala Pro
 20 25 30
 Ser Leu Arg Leu Arg Cys Thr Pro Thr Ser Arg Pro Ser Ser Ser
 35 40 45
 Trp Ala Ala Ala Val Ser Ser Ala Ser Arg Leu Val Glu Pro Asp
 50 55 60
 Pro Asn Gln Pro Leu Ile Asn Pro Leu Asn Leu Val Gly Pro Glu
 65 70 75
 Met Ser Asn Leu Thr Ser Asn Ile Arg Ser Leu Leu Gly Ser Gly
 80 85 90
 His Pro Ser Leu Asp Thr Val Ala Lys Tyr Tyr Val Gln Ser Glu
 95 100 105
 Gly Lys His Ile Arg Pro Leu Met Val Leu Leu Met Ala Gln Ala
 110 115 120
 Thr Glu Val Ala Pro Lys Val Gln Gly Trp Glu Lys Val Val Glu
 125 130 135
 Val Pro Val Asn Glu Gly Leu Ala Pro Pro Glu Val Leu Asn Asp
 140 145 150
 Lys Asn Pro Asp Met Met Asn Met Arg Ser Gly Pro Leu Thr Lys
 155 160 165
 Asp Gly Glu Ile Glu Gly Gln Thr Ser Asn Ile Leu Ala Ser Gln
 170 175 180
 Arg Arg Leu Ala Glu Ile Thr Glu Met Ile His Ala Ala Ser Leu
 185 190 195
 Leu His Asp Asp Val Ile Asp Ala Ser Glu Thr Arg Arg Asn Ala
 200 205 210
 Pro Ser Gly Asn Gln Ala Phe Gly Asn Lys Met Ala Ile Leu Ala
 215 220 225

Gly Asp Phe Leu Leu Gly Arg Ala Ser Val Ala Leu Ala Arg Leu
230 235 240
Arg Asn Pro Glu Val Ile Glu Leu Leu Ala Thr Val Ile Ala Asn
245 250 255
Leu Val Glu Gly Glu Phe Met Gin Leu Lys Asn Thr Val Asp Asp
260 265 270
Ala Ile Glu Ala Thr Ala Thr Gin Glu Thr Phe Asp Tyr Tyr Leu
275 280 285
Gln Lys Thr Tyr Leu Lys Thr Ala Ser Leu Ile Ala Lys Ser Cys
290 295 300
Arg Ala Ser Ala Leu Leu Gly Gly Ala Thr Pro Glu Val Ala Asp
305 310 315
Ala Ala Tyr Ala Tyr Gly Arg Asn Leu Gly Leu Ala Phe Gin Ile
320 325 330
Val Asp Asp Met Leu Asp Tyr Thr Val Ser Ala Thr Asp Leu Gly
335 340 345
Lys Pro Ala Gly Ala Asp Leu Gin Leu Gly Leu Ala Thr Ala Pro
350 355 360
Ala Leu Phe Ala Trp Lys His His Ala Glu Leu Gly Pro Met Ile
365 370 375
Lys Arg Lys Phe Ser Asp Pro Gly Asp Val Glu Arg Ala Arg Glu
380 385 390
Leu Val Glu Lys Ser Asp Gly Leu Glu Lys Thr Arg Ala Leu Ala
395 400 405
Glu Glu Tyr Ala Gln Lys Ala Leu Asp Ala Ile Arg Thr Phe Pro
410 415 420
Glu Ser Pro Ala Arg Lys Ala Leu Glu Gln Leu Thr Asp Lys Val
425 430 435
Leu Thr Arg Ser Arg
440

delete all underlines (global error)

<210> 3

<211> 24

<212> DNA

<213> Artificial Sequence

← see item 11 on Error Summary Sheet

<400> 3

see item 9 on Error Summary Sheet

aaggatcctn ythcaygayg aygt 24

<210> 4

<211> 17

<212> DNA

<213> Artificial Sequence

item 11

delete underlines

<400> 4

item 9

arytonadra aytoncc 17

<210> 5

<211> 21

<212> DNA

<213> Artificial Sequence

item 11

delete underlines

<400> 5

gagaccagac gaaacgcacc a 21

<210> 6

<211> 21

09/830,111B

5

<212> DNA

<213> Artificial Sequence

item 11

<400> 6

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21

delete underlines

<210> 7

<211> 26

<212> DNA

<213> Artificial Sequence

item 11

<400> 7

aacatatggc ctcaccagca ctgcgg

26

delete underlines

<210> 8

<211> 29

<212> DNA

<213> Artificial Sequence

item 11

<400> 8

aagaattcct atcttgacct agtcaacac

29

delete underlines